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☐ 1: NP_660187. ATP-binding casse...[gi:21729876]

BLink, Domains, Links

LOCUS NP_660187 1344 aa linear PRI 07-SEP-2003
 DEFINITION ATP-binding cassette, sub-family C, member 11 isoform b;
 multi-resistance protein 8; ATP-binding cassette transporter MRP8;
 ATP-binding cassette protein C11 [Homo sapiens].
 ACCESSION NP_660187
 VERSION NP_660187.1 GI:21729876
 DBSOURCE REFSEQ: accession [NM_145186.1](#)
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (residues 1 to 1344)
 AUTHORS Turriziani, O., Schuetz, J.D., Focher, F., Scagnolari, C., Sampath, J.,
 Adachi, M., Bambacioni, F., Riva, E. and Antonelli, G.
 TITLE Impaired 2',3'-dideoxy-3'-thiacytidine accumulation in
 T-lymphoblastoid cells as a mechanism of acquired resistance
 independent of multidrug resistant protein 4 with a possible role
 for ATP-binding cassette C11
 JOURNAL Biochem. J. 368 (Pt 1), 325-332 (2002)
 MEDLINE 22304623
 PUBMED 12133003
 REMARK GeneRIF: Impaired 2',3'-dideoxy-3'-thiacytidine accumulation in
 T-lymphoblastoid cells as a mechanism of acquired resistance
 independent of multidrug resistant protein 4 with a possible role
 for ATP-binding cassette C11.
 REFERENCE 2 (residues 1 to 1344)
 AUTHORS Yabuuchi, H., Shimizu, H., Takayanagi, S. and Ishikawa, T.
 TITLE Multiple splicing variants of two new human ATP-binding cassette
 transporters, ABCC11 and ABCC12
 JOURNAL Biochem. Biophys. Res. Commun. 288 (4), 933-939 (2001)
 MEDLINE 21547789
 PUBMED 11688999
 REMARK GeneRIF: alternative splice variants and gene expression
 REFERENCE 3 (residues 1 to 1344)
 AUTHORS Bera, T.K., Lee, S., Salvatore, G., Lee, B. and Pastan, I.
 TITLE MRP8, a new member of ABC transporter superfamily, identified by
 EST database mining and gene prediction program, is highly
 expressed in breast cancer
 JOURNAL Mol. Med. 7 (8), 509-516 (2001)
 MEDLINE 21475973
 PUBMED 11591886
 REFERENCE 4 (residues 1 to 1344)
 AUTHORS Tammur, J., Prades, C., Arnould, I., Rzhetsky, A., Hutchinson, A.,
 Adachi, M., Schuetz, J.D., Swoboda, K.J., Ptacek, L.J., Rosier, M.,
 Dean, M. and Allikmets, R.
 TITLE Two new genes from the human ATP-binding cassette transporter

superfamily, ABCC11 and ABCC12, tandemly duplicated on chromosome 16q12

JOURNAL Gene 273 (1), 89-96 (2001)
 MEDLINE [21376129](#)
 PUBMED [11483364](#)

REFERENCE 5 (residues 1 to 1344)
 AUTHORS Dean,M., Rzhetsky,A. and Allikmets,R.
 TITLE The human ATP-binding cassette (ABC) transporter superfamily
 JOURNAL Genome Res. 11 (7), 1156-1166 (2001)
 MEDLINE [21329047](#)
 PUBMED [11435397](#)

COMMENT REVIEWED [REFSEQ](#): This record has been curated by NCBI staff. The reference sequence was derived from [AF411579.1](#).

Summary: The protein encoded by this gene is a member of the superfamily of ATP-binding cassette (ABC) transporters. ABC proteins transport various molecules across extra- and intra-cellular membranes. ABC genes are divided into seven distinct subfamilies (ABCC1, MDR/TAP, MRP, ALD, OABP, GCN20, White). This ABC full transporter is a member of the MRP subfamily which is involved in multi-drug resistance. It is expressed at low levels in all tissues, except kidney, spleen, and colon. This gene and family member ABCC12 are determined to be derived by duplication and are both localized to chromosome 16q12.1. Their chromosomal localization, potential function, and expression patterns identify them as candidates for paroxysmal kinesigenic choreoathetosis, a disorder characterized by attacks of involuntary movements and postures, chorea, and dystonia. Multiple alternatively spliced transcript variants have been described for this gene.

Transcript Variant: This variant (3) lacks an alternate in-frame exon compared to variant 1, resulting in a shorter protein (isoform b), compared to isoform a.

FEATURES

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 /chromosome="16"
 /map="16q12.1"

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 /note="multi-resistance protein 8; ATP-binding cassette transporter MRP8; ATP-binding cassette protein C11"

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 /note="MdlB"
 /db_xref="CDD:COG1132"

Region 853..1338
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 /note="MdlB"
 /db_xref="CDD:COG1132"

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 /db_xref="LocusID:85320"
 /db_xref="MIM:607040"

ORIGIN

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181 piliipkile yseeqlgnvv hgvglcalf lsecvkslsf ssswiinqrt airfraavss
241 fafekliqfk svihitsgea isfftgdvny lfegvcygp1 vlitcaslvi csissyfiig
301 ytafiaailcy llvfplavfm trmavkaqhh tsevsdqrir vtsevltcik likmytwekp
361 fakiiedlrr kerklllekg lvqsltsitl fiipvtatav wvlihtslkl kltasmafsm
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721 qkkgkyaqli qkmhkeatsd mlqdtakiae kpkvesqala tsleeslgn avpehqltqe
781 eemeegslsw rvyhhyiqaa ggymvsciif ffvvlivflt ifsfwwlsyw leqsgtss
841 resngtmadl gniadnpqls fyqlvyglna lllicvgvcs sgiftkvtrk astalhnklf
901 nkvfrcpmsf fdtipigrll ncfagdleql dqllpifseq flvlsmlvia vllivsvlsp
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1261 ilideatasi dmetdtliqr tireafqgct vlviahrvtt vlncdhilvm gngkvvefdr
1321 pevlrkkpgs lfaalmatat sslr

//

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Sep 4 2003 10:24:36

FASTA searches a protein or DNA sequence data bank
version 3.3t05 March 30, 2000

Please cite:

W.R. Pearson & D.J. Lipman PNAS (1988) 85:2444-2448

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>seqid24
vs /tmp/fastaHAACJayWj library
searching /tmp/fastaHAACJayWj library

1344 residues in 1 sequences

FASTA (3.34 January 2000) function [optimized, BL50 matrix (15:-5)] ktup: 2
join: 40, opt: 28, gap-pen: -12/-2, width: 16
Scan time: 0.034

The best scores are:

NP_660187 ACCESSION:NP_660187 NID: gi 21729876 re (1344) 4838 opt

>>NP_660187 ACCESSION:NP_660187 NID: gi 21729876 ref NP_ (1344 aa)

initn: 7156 initl: 4838 opt: 4838

Smith-Waterman score: 7274; 85.311% identity in 1382 aa overlap (1-1219:1-1344)

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NP_660	MTRKRTYWPNSSGGLVNRGIDIGDDMVSGLIYKTYTLQDGPWSQQERNPEAPGRAAVPP					

	70	80	90	100	110	120
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NP_660	WGKYDAALRTMIPFRPKPRFPAPQPLDNAGLFSYLTVSWLTPLMIQSLRSRLDENTIPPL					

	130	140	150	160	170	180
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	190	200	210	220	230	240
seqid2	PILIIPKILEYSEEQLGNVHVHGVGLCFALFLSECVKSLSFSSSWIINQRTAIRFQAAVSS					
NP_660	PILIIPKILEYSEEQLGNVHVHGVGLCFALFLSECVKSLSFSSSWIINQRTAIRFRAAVSS					

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      550      560      570      580      590      600
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